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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/884,696

DATE: 09/06/2001

TIME: 15:20:38

Input Set : A:\481-06.app

Output Set: N:\CRF3\09062001\I884696.raw

PS

3 <110> APPLICANT: GEORGE, LISLE W
 4 ANGELOS, JOHN A
 5 HESS, JOHN F
 7 <120> TITLE OF INVENTION: MORAXELLA BOVIS CYTOTOXIN, CYTOTOXIN GENE, ANTIBODIES
 8 AND VACCINES FOR PREVENTION AND TREATMENT OF MORAXELLA
 9 BOVIS INFECTIONS
 11 <130> FILE REFERENCE: 481.06
 13 <140> CURRENT APPLICATION NUMBER: 09/884,696
 14 <141> CURRENT FILING DATE: 2001-06-19
 16 <160> NUMBER OF SEQ ID NOS: 41
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2784
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Moraxella bovis
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(2781)
 29 <400> SEQUENCE: 1

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31	Met Ser Asn Ile Asn Val Ile Lys Ser Asn Ile Gln Ala Gly Leu Asn	
32	1 5 10 15	
34	tca aca aag tct gga tta aaa aat ctt tac ttg gct att ccc aaa gat	96
35	Ser Thr Lys Ser Gly Leu Lys Asn Leu Tyr Leu Ala Ile Pro Lys Asp	
36	20 25 30	
38	tat gat ccg caa aaa ggt ggg act tta aat gat ttt att aaa gct gct	144
39	Tyr Asp Pro Gln Lys Gly Gly Thr Leu Asn Asp Phe Ile Lys Ala Ala	
40	35 40 45	
42	gat gaa tta ggt att gct cgt tta gca gaa gag cct aat cac act gaa	192
43	Asp Glu Leu Gly Ile Ala Arg Leu Ala Glu Glu Pro Asn His Thr Glu	
44	50 55 60	
46	aca gca aaa aaa tct gtt gac aca gta aat cag ttt ctc tct ctc aca	240
47	Thr Ala Lys Lys Ser Val Asp Thr Val Asn Gln Phe Leu Ser Leu Thr	
48	65 70 75 80	
50	caa act ggt att gct att tct gca aca aaa tta gaa aag ttc tta caa	288
51	Gln Thr Gly Ile Ala Ile Ser Ala Thr Lys Leu Glu Lys Phe Leu Gln	
52	85 90 95	
54	aaa cat tct acc aat aag tta gcc aaa ggg tta gac agt gta gaa aat	336
55	Lys His Ser Thr Asn Lys Leu Ala Lys Gly Leu Asp Ser Val Glu Asn	
56	100 105 110	
58	att gat cgt aaa tta ggt aaa gca agt aat gta tta tca aca tta agc	384
59	Ile Asp Arg Lys Leu Gly Lys Ala Ser Asn Val Leu Ser Thr Leu Ser	
60	115 120 125	
62	tct ttt ttg ggc act gca tta gcg ggt ata gaa ctt gat tct tta atc	432
63	Ser Phe Leu Gly Thr Ala Leu Ala Gly Ile Glu Leu Asp Ser Leu Ile	
64	130 135 140	
66	aaa aaa ggt gat gct gca cct gat gct ttg gct aaa gct agt att gac	480

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67 Lys Lys Gly Asp Ala Ala Pro Asp Ala Leu Ala Lys Ala Ser Ile Asp
68 145 150 155 160
70 ttg att aat gag ata att ggt aat cta tct cag agt act caa acg att 528
71 Leu Ile Asn Glu Ile Ile Gly Asn Leu Ser Gln Ser Thr Gln Thr Ile
72 165 170 175
74 gaa gca ttt tct tca cag tta gca aag tta ggt tct act ata tcg cag 576
75 Glu Ala Phe Ser Ser Gln Leu Ala Lys Leu Gly Ser Thr Ile Ser Gln
76 180 185 190
78 gct aaa ggc ttc tct aat ata gga aac aag ttg caa aac tta aat ttt 624
79 Ala Lys Gly Phe Ser Asn Ile Gly Asn Lys Leu Gln Asn Leu Asn Phe
80 195 200 205
82 tct aaa aca aat ctt ggt ttg gaa ata att act ggt ttg cta tca ggc 672
83 Ser Lys Thr Asn Leu Gly Leu Glu Ile Ile Thr Gly Leu Leu Ser Gly
84 210 215 220
86 att tct gca ggc ttt gct tta gcg gat aaa aat gca tcg act ggc aaa 720
87 Ile Ser Ala Gly Phe Ala Leu Ala Asp Lys Asn Ala Ser Thr Gly Lys
88 225 230 235 240
90 aaa gtt gct gca ggt ttt gaa tta agc aat caa gtt att ggt aat gta 768
91 Lys Val Ala Ala Gly Phe Glu Leu Ser Asn Gln Val Ile Gly Asn Val
92 245 250 255
94 aca aaa gca att tct tca tat gtt tta gca caa cgt gtt gct gct ggt 816
95 Thr Lys Ala Ile Ser Ser Tyr Val Leu Ala Gln Arg Val Ala Ala Gly
96 260 265 270
98 cta tca act act ggt gct gtt gct gct tta att act tca tcg att atg 864
99 Leu Ser Thr Thr Gly Ala Val Ala Ala Leu Ile Thr Ser Ser Ile Met
100 275 280 285
102 ttg gca att agt cct ttg gca ttt atg aat gca gca gat aaa ttc aat 912
103 Leu Ala Ile Ser Pro Leu Ala Phe Met Asn Ala Ala Asp Lys Phe Asn
104 290 295 300
106 cat gct aat gct ctt gat gag ttt gca aaa caa ttc cga aaa ttt ggc 960
107 His Ala Asn Ala Leu Asp Glu Phe Ala Lys Gln Phe Arg Lys Phe Gly
108 305 310 315 320
110 tat gat ggg gat cat tta ttg gct gaa tat cag cgt ggt gtg ggt act 1008
111 Tyr Asp Gly Asp His Leu Leu Ala Glu Tyr Gln Arg Gly Val Gly Thr
112 325 330 335
114 att gaa gct tca tta act aca att agt acg gca tta ggt gca gtt tct 1056
115 Ile Glu Ala Ser Leu Thr Thr Ile Ser Thr Ala Leu Gly Ala Val Ser
116 340 345 350
118 gct ggt gtt tcc gct gct gct gta gga tct gct gtt ggt gca ccg att 1104
119 Ala Gly Val Ser Ala Ala Ala Val Gly Ser Ala Val Gly Ala Pro Ile
120 355 360 365
122 gca cta tta gtt gca ggt gtt aca gga ttg atc tct gga att tta gaa 1152
123 Ala Leu Leu Val Ala Gly Val Thr Gly Leu Ile Ser Gly Ile Leu Glu
124 370 375 380
126 gcg tct aaa cag gca atg ttt gaa agt gtt gct aac cgt tta caa ggt 1200
127 Ala Ser Lys Gln Ala Met Phe Glu Ser Val Ala Asn Arg Leu Gln Gly
128 385 390 395 400
130 aaa att tta gag tgg gaa aag caa aat ggc ggt cag aac tat ttt gat 1248
131 Lys Ile Leu Glu Trp Glu Lys Gln Asn Gly Gly Gln Asn Tyr Phe Asp

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132		405		410		415		
134	aaa ggc tat	gat tct cgt	tat gct gct	tat tta gct	aat aac	tta aaa	1296	
135	Lys Gly Tyr	Asp Ser Arg	Tyr Ala Ala	Tyr Leu Ala	Asn Asn	Leu Lys		
136		420		425		430		
138	ttt ttg tct	gag cta aat	aaa gag ttg	gaa gct gaa	cgt gtt	att gca	1344	
139	Phe Leu Ser	Glu Leu Asn	Lys Glu Leu	Glu Ala Glu	Arg Val	Ile Ala		
140		435		440		445		
142	atc acc caa	caa cgt tgg	gat aat aat	att ggt gag	tta gca	ggt att	1392	
143	Ile Thr Gln	Gln Arg Trp	Asp Asn Asn	Ile Gly Glu	Leu Ala	Gly Ile		
144		450		455		460		
146	acc aaa ttg	ggt gaa cgc	att aag agc	gga aaa gct	tat gca	gat gct	1440	
147	Thr Lys Leu	Gly Glu Arg	Ile Lys Ser	Gly Lys Ala	Tyr Ala	Asp Ala		
148	465		470		475	480		
150	ttt gaa gat	ggc aag aaa	gtt gaa gct	ggt tcc aat	att act	ttg gat	1488	
151	Phe Glu Asp	Gly Lys Lys	Val Glu Ala	Gly Ser Asn	Ile Thr	Leu Asp		
152		485		490		495		
154	gct aaa act	ggt atc ata	gac att agt	aat tca aat	ggg aaa	aaa acg	1536	
155	Ala Lys Thr	Gly Ile Ile	Asp Ile Ser	Asn Ser Asn	Gly Lys	Lys Thr		
156		500		505		510		
158	caa gcg ttg	cat ttc act	tcg cct ttg	tta aca gca	gga act	gaa tca	1584	
159	Gln Ala Leu	His Phe Thr	Ser Pro Leu	Leu Leu Thr	Ala Gly	Thr Glu		
160		515		520		525		
162	cgt gaa cgt	tta act aat	ggt aaa tac	tct tat att	aat aag	tta aaa	1632	
163	Arg Glu Arg	Leu Thr Asn	Gly Lys Tyr	Ser Tyr Ile	Asn Lys	Leu Lys		
164		530		535		540		
166	ttc gga cgt	gta aaa aac	tgg caa gtt	aca gat gga	gag gct	agt tct	1680	
167	Phe Gly Arg	Val Lys Asn	Trp Gln Val	Thr Asp Gly	Glu Ala	Ser Ser		
168	545		550		555	560		
170	aaa tta gat	ttc tct aaa	gtt att cag	cgt gta gcc	gag aca	gaa ggc	1728	
171	Lys Leu Asp	Phe Ser Lys	Val Ile Gln	Arg Val Ala	Glu Thr	Glu Gly		
172		565		570		575		
174	aca gac gag	att ggt cta	ata gta aat	gca aaa gct	ggc aat	gac gat	1776	
175	Thr Asp Glu	Ile Gly Leu	Ile Val Asn	Ala Lys Ala	Gly Asn	Asp Asp		
176		580		585		590		
178	atc ttt gtt	ggt caa ggt	aaa atg aat	att gat ggt	gga gat	gga cac	1824	
179	Ile Phe Val	Gly Gln Gly	Lys Met Asn	Ile Asp Gly	Gly Asp	Gly His		
180		595		600		605		
182	gat cgt gtc	ttc tat agt	aaa gac gga	gga ttt ggt	aat att	act gta	1872	
183	Asp Arg Val	Phe Tyr Ser	Lys Asp Gly	Gly Phe Gly	Asn Ile	Thr Val		
184		610		615		620		
186	gat ggt acg	agt gca aca	gaa gca ggc	agt tat aca	gtt aat	cgt aag	1920	
187	Asp Gly Thr	Ser Ala Thr	Glu Ala Gly	Ser Tyr Thr	Val Asn	Arg Lys		
188	625		630		635	640		
190	gtt gct cga	ggt gat atc	tac cat gaa	gtt gtg aag	cgt caa	gaa acc	1968	
191	Val Ala Arg	Gly Asp Ile	Tyr His Glu	Val Val Lys	Arg Gln	Glu Thr		
192		645		650		655		
194	aag gtg ggt	aaa cgt act	gaa act atc	cag tat cgt	gat tat	gaa tta	2016	
195	Lys Val Gly	Lys Arg Thr	Glu Thr Ile	Gln Tyr Arg	Asp Tyr	Glu Leu		
196		660		665		670		

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198 aga aaa gtt ggg tat ggt tat cag tct acc gat aat ttg aaa tca gta 2064
199 Arg Lys Val Gly Tyr Gly Tyr Gln Ser Thr Asp Asn Leu Lys Ser Val
200      675      680      685
202 gaa gaa gta att ggt tct caa ttt aat gat gta ttc aaa ggt tct aaa 2112
203 Glu Glu Val Ile Gly Ser Gln Phe Asn Asp Val Phe Lys Gly Ser Lys
204      690      695      700
206 ttc aac gac ata ttc cat agt ggt gaa ggt gat gat tta ctc gat ggt 2160
207 Phe Asn Asp Ile Phe His Ser Gly Glu Gly Asp Asp Leu Leu Asp Gly
208 705      710      715      720
210 ggt gct ggt gac gac cgc ttg ttt ggt ggt aaa ggc aac gat cga ctt 2208
211 Gly Ala Gly Asp Asp Arg Leu Phe Gly Gly Lys Gly Asn Asp Arg Leu
212      725      730      735
214 tct gga gat gaa ggc gat gat tta ctc gat ggc ggt tct ggt gat gat 2256
215 Ser Gly Asp Glu Gly Asp Asp Leu Leu Asp Gly Gly Ser Gly Asp Asp
216      740      745      750
218 gta tta aat ggt ggt gct ggt aat gat gtc tat atc ttt cgg aaa ggt 2304
219 Val Leu Asn Gly Gly Ala Gly Asn Asp Val Tyr Ile Phe Arg Lys Gly
220      755      760      765
222 gat ggt aat gat act ttg tac gat ggc acg ggc aat gat aaa tta gca 2352
223 Asp Gly Asn Asp Thr Leu Tyr Asp Gly Thr Gly Asn Asp Lys Leu Ala
224      770      775      780
226 ttt gca gat gca aat ata tct gat att atg att gaa cgt acc aaa gag 2400
227 Phe Ala Asp Ala Asn Ile Ser Asp Ile Met Ile Glu Arg Thr Lys Glu
228 785      790      795      800
230 ggt att ata gtt aaa cga aat gat cat tca ggt agt att aac ata cca 2448
231 Gly Ile Ile Val Lys Arg Asn Asp His Ser Gly Ser Ile Asn Ile Pro
232      805      810      815
234 aga tgg tac ata aca tca aat tta caa aat tat caa agt aat aaa aca 2496
235 Arg Trp Tyr Ile Thr Ser Asn Leu Gln Asn Tyr Gln Ser Asn Lys Thr
236      820      825      830
238 gat cat aaa att gag caa cta att ggt aaa gat ggt agt tat atc act 2544
239 Asp His Lys Ile Glu Gln Leu Ile Gly Lys Asp Gly Ser Tyr Ile Thr
240      835      840      845
242 tcc gat caa att gat aaa att ttg caa gat aag aaa gat ggt aca gta 2592
243 Ser Asp Gln Ile Asp Lys Ile Leu Gln Asp Lys Lys Asp Gly Thr Val
244      850      855      860
246 att aca tct caa gaa ttg aaa aag ctt gct gat gag aat aag agc caa 2640
247 Ile Thr Ser Gln Glu Leu Lys Lys Leu Ala Asp Glu Asn Lys Ser Gln
248 865      870      875      880
250 aaa tta tct gct tcg gac att gca agt agc tta aat aag cta gtt ggg 2688
251 Lys Leu Ser Ala Ser Asp Ile Ala Ser Ser Leu Asn Lys Leu Val Gly
252      885      890      895
254 tca atg gca cta ttt ggt aca gca aat agt gtg agt tct aac gcc tta 2736
255 Ser Met Ala Leu Phe Gly Thr Ala Asn Ser Val Ser Ser Asn Ala Leu
256      900      905      910
258 cag cca att aca caa cca act caa gga att ttg gct cca agt gtt tag 2784
259 Gln Pro Ile Thr Gln Pro Thr Gln Gly Ile Leu Ala Pro Ser Val
260      915      920      925
263 <210> SEQ ID NO: 2

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264 <211> LENGTH: 927
265 <212> TYPE: PRT
266 <213> ORGANISM: Moraxella bovis
268 <400> SEQUENCE: 2
269 Met Ser Asn Ile Asn Val Ile Lys Ser Asn Ile Gln Ala Gly Leu Asn
270 1 5 10 15
272 Ser Thr Lys Ser Gly Leu Lys Asn Leu Tyr Leu Ala Ile Pro Lys Asp
273 20 25 30
275 Tyr Asp Pro Gln Lys Gly Gly Thr Leu Asn Asp Phe Ile Lys Ala Ala
276 35 40 45
278 Asp Glu Leu Gly Ile Ala Arg Leu Ala Glu Glu Pro Asn His Thr Glu
279 50 55 60
281 Thr Ala Lys Lys Ser Val Asp Thr Val Asn Gln Phe Leu Ser Leu Thr
282 65 70 75 80
284 Gln Thr Gly Ile Ala Ile Ser Ala Thr Lys Leu Glu Lys Phe Leu Gln
285 85 90 95
287 Lys His Ser Thr Asn Lys Leu Ala Lys Gly Leu Asp Ser Val Glu Asn
288 100 105 110
290 Ile Asp Arg Lys Leu Gly Lys Ala Ser Asn Val Leu Ser Thr Leu Ser
291 115 120 125
293 Ser Phe Leu Gly Thr Ala Leu Ala Gly Ile Glu Leu Asp Ser Leu Ile
294 130 135 140
296 Lys Lys Gly Asp Ala Ala Pro Asp Ala Leu Ala Lys Ala Ser Ile Asp
297 145 150 155 160
299 Leu Ile Asn Glu Ile Ile Gly Asn Leu Ser Gln Ser Thr Gln Thr Ile
300 165 170 175
302 Glu Ala Phe Ser Ser Gln Leu Ala Lys Leu Gly Ser Thr Ile Ser Gln
303 180 185 190
305 Ala Lys Gly Phe Ser Asn Ile Gly Asn Lys Leu Gln Asn Leu Asn Phe
306 195 200 205
308 Ser Lys Thr Asn Leu Gly Leu Glu Ile Ile Thr Gly Leu Leu Ser Gly
309 210 215 220
311 Ile Ser Ala Gly Phe Ala Leu Ala Asp Lys Asn Ala Ser Thr Gly Lys
312 225 230 235 240
314 Lys Val Ala Ala Gly Phe Glu Leu Ser Asn Gln Val Ile Gly Asn Val
315 245 250 255
317 Thr Lys Ala Ile Ser Ser Tyr Val Leu Ala Gln Arg Val Ala Ala Gly
318 260 265 270
320 Leu Ser Thr Thr Gly Ala Val Ala Ala Leu Ile Thr Ser Ser Ile Met
321 275 280 285
323 Leu Ala Ile Ser Pro Leu Ala Phe Met Asn Ala Ala Asp Lys Phe Asn
324 290 295 300
326 His Ala Asn Ala Leu Asp Glu Phe Ala Lys Gln Phe Arg Lys Phe Gly
327 305 310 315 320
329 Tyr Asp Gly Asp His Leu Leu Ala Glu Tyr Gln Arg Gly Val Gly Thr
330 325 330 335
332 Ile Glu Ala Ser Leu Thr Thr Ile Ser Thr Ala Leu Gly Ala Val Ser
333 340 345 350
335 Ala Gly Val Ser Ala Ala Ala Val Gly Ser Ala Val Gly Ala Pro Ile

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:1098 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1873 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:2825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41